gembloux agro bio tech

WBI Wallonie-Bruxelles International

Université de Liège

Slovenia, November 22

Integration / blending of external information into genetic / genomic evaluations

J. Vandenplas[1,2], N. Gengler[1]

[1]University of Liège, Gembloux Agro-Bio Tech, Belgium

[2]National Fund for Scientific Research, Brussels, Belgium

Introduction

- Most reliable EBV if estimated from all available sources
- Most situations
  - Multiple sources (e.g., dairy breeds)
    - Traditional genetic evaluations
    - International second step (Interbull)

  ➔ Animals with few (or no) local data: low accuracy
  - Development of genomic selection

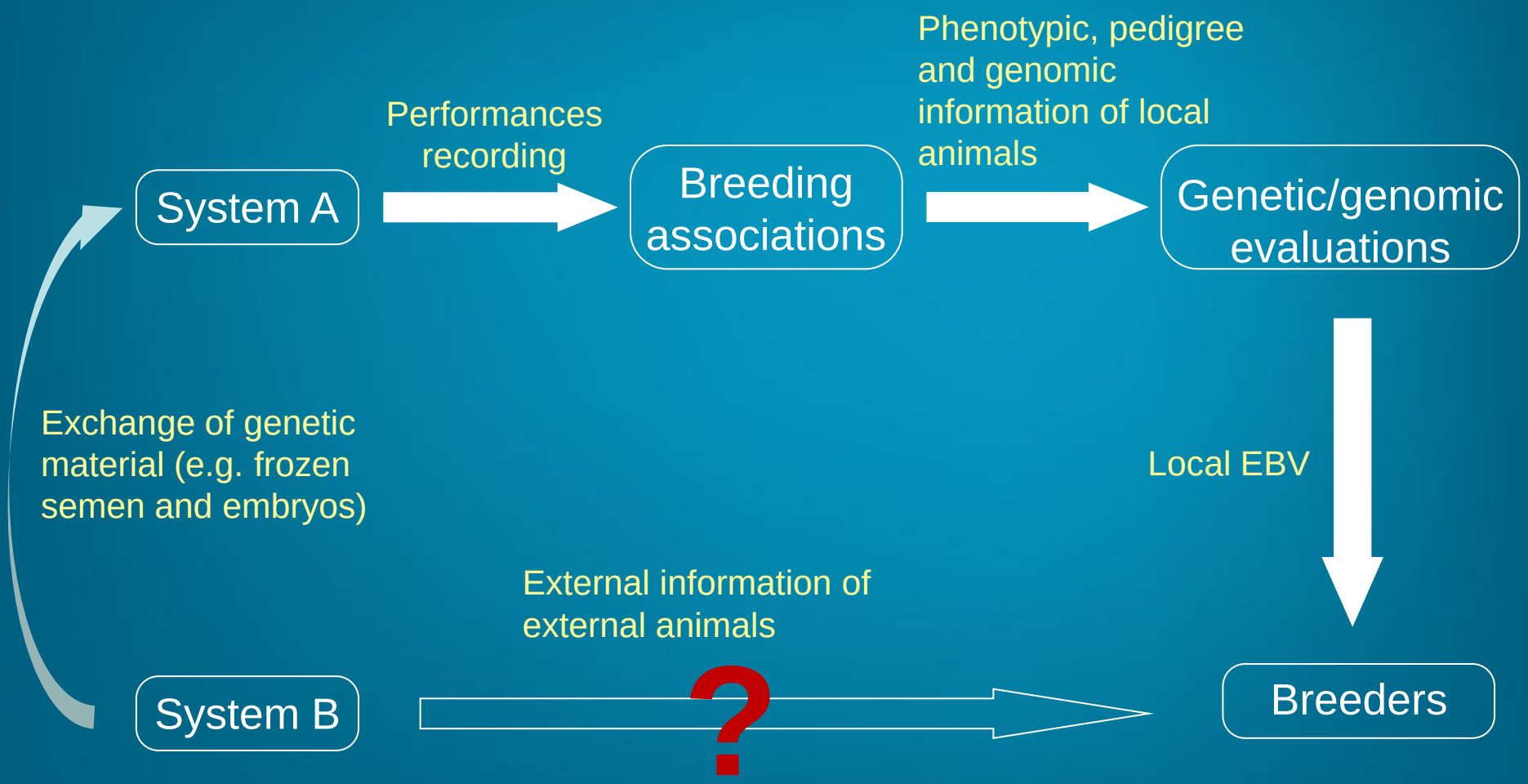
    ➔New genomic information sources

➔ Strategies for integration / blending of those multiple sources of external information

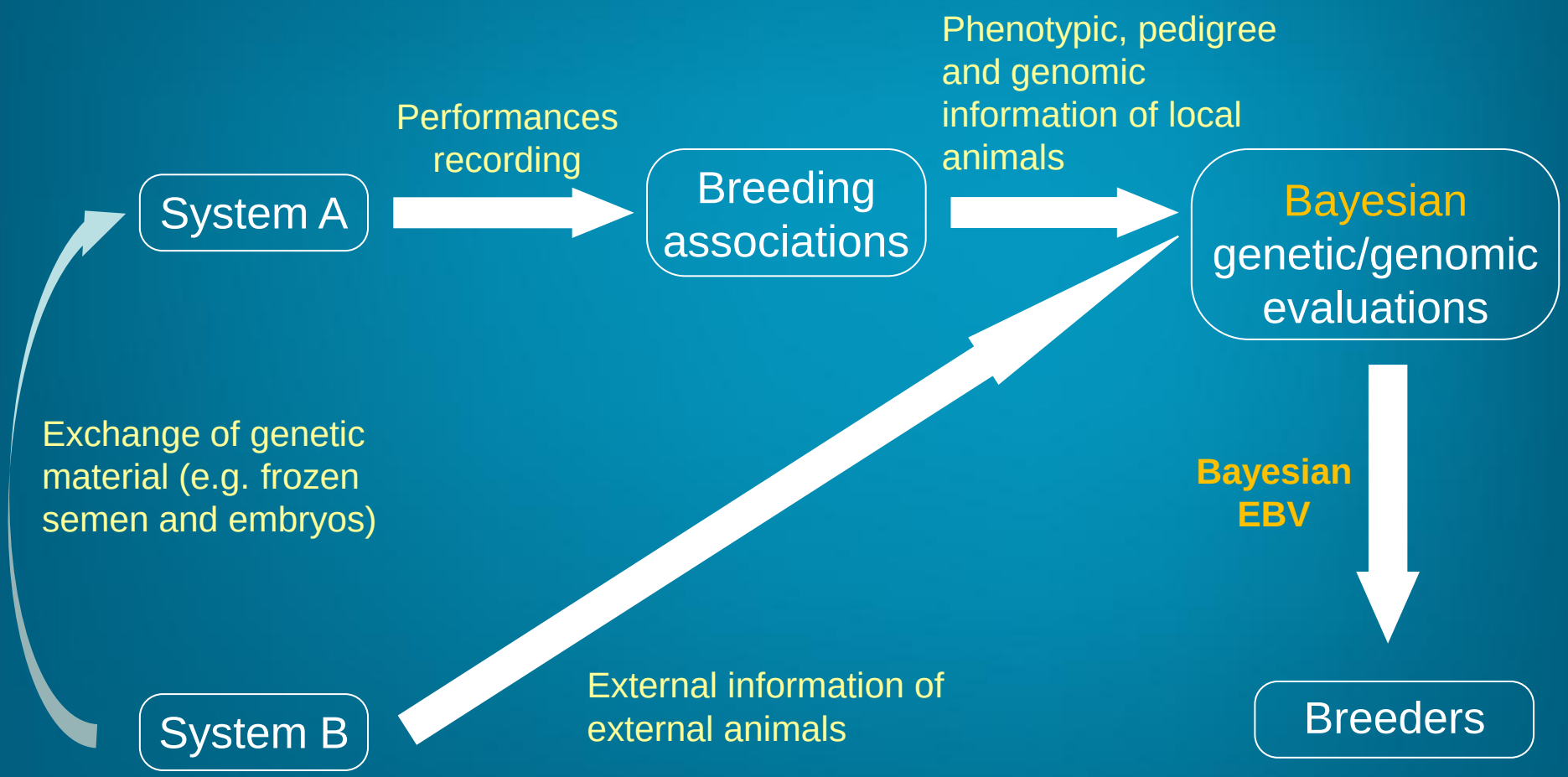
Introduction

- Single-step genomic evaluation (ssGBLUP)
  - ➔ Genomic, pedigree and phenotypic information considered simultaneously
- Current limitation
  - Only available local records used
  - ➔ Disadvantage compared to multi-steps methods using e.g. MACE-EBV as a way to access to external phenotypic information

Current situation



Possible solution



Aim

To integrate/blend multiple *a priori* known external information into a local genetic/genomic evaluation

➔ Using a Bayesian approach

- Based on
  - Legarra et al. (2007)
  - Quaas and Zhang (2006)
  - Vandenplas and Gengler (2012a, 2012b)
  - Vandenplas et al. (2012a, 2012b)

External information

- Most situations
  - EBV and REL from other genetic evaluations
  - Information not taken into account by a local (ssG)BLUP
    - ➔Not an external genomic evaluation
    - ➔No double-counting between local and external evaluations
  - Only available for some animals
    - Having, or not, phenotypic information in the local (ssG)BLUP
    - Present in the pedigree of the local (ssG)BLUP

Regular (ssG)BLUP

- Mixed model equations

$$\begin{bmatrix} \mathbf{X'R^{-1}X} & \mathbf{X'R^{-1}Z} \\ \mathbf{Z'R^{-1}X} & \mathbf{Z'R^{-1}Z} + \mathbf{G^{*-1}} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_L \\ \hat{\mathbf{u}}_L \end{bmatrix} = \begin{bmatrix} \mathbf{X'R^{-1}y}_L \\ \mathbf{Z'R^{-1}y}_L \end{bmatrix}$$

  - $\mathbf{G}^{*-1}$: Inverse of (combined genomic-) pedigree based (co)variances matrix
  - $\mathbf{y}_L$: vector of local observations
  - $\hat{\boldsymbol{\beta}}_L$: vector of estimated local fixed effects
  - $\hat{\mathbf{u}}_L$: vector of estimated local (G)EBV
  - $p(\mathbf{u}_L) = MVN(\mathbf{0}, \mathbf{G}^*)$

Integration of one source

- Assumption: Conditional distribution of $\mathbf{u}_L$

$$p(\mathbf{u}_L | \mathbf{y}_E) = MVN(\hat{\mathbf{u}}_E, \mathbf{D})$$

  - $\mathbf{y}_E$: unavailable vector of external observations
  - $\hat{\mathbf{u}}_E$: vector of external EBV
  - $\mathbf{D}$: prediction error (co)variances matrix of $\hat{\mathbf{u}}_E$

- Issue: only available for some animals

➔ $\hat{\mathbf{u}}_E$ and $\mathbf{D}$: (partially) unknown

Integration of one source

- Estimation of $\hat{\mathbf{u}}_E$
  - Available: External EBV of external animals ($\hat{\mathbf{u}}^*_{EE}$)
  - Local animals: prediction of external EBV ($\hat{\mathbf{u}}_{EL}$)

$$p(\hat{\mathbf{u}}_{EL} \mid \hat{\mathbf{u}}^*_{EE}) = MVN\left(\mathbf{G}_{LE}\mathbf{G}^{-1}_{EE}\hat{\mathbf{u}}^*_{EE}, (\mathbf{G}^{EE})^{-1}\right)$$

➔ $\hat{\mathbf{u}}_E = \begin{bmatrix} \hat{\mathbf{u}}_{EL} \\ \hat{\mathbf{u}}^*_{EE} \end{bmatrix}$

Predicted external EBV

Available external EBV

➔Correct propagation of external information

Integration of one source

- Estimation of $\mathbf{D}$

$$\mathbf{D}^{-1} = \mathbf{G}^{-1} + \mathbf{\Lambda}$$

  - $\mathbf{G}^{-1} = \mathbf{A}^{-1} \otimes \mathbf{G}_0^{-1}$: Inverse of genetic (co)variances matrix of $\hat{\mathbf{u}}_E$
  - $\mathbf{\Lambda} = \text{block diag}(\mathbf{\Delta}_i \mathbf{G}_0^{-1} \mathbf{\Delta}_i)$; $i = 1, ..., n$ animals

$$\begin{cases} \text{For external animals} : \mathbf{\Delta}_i = \text{diag}(\sqrt{\text{REL}_{ij} / (1 - \text{REL}_{ij})}); \; j = 1, ..., t \text{ traits} \\ \text{For animals with only local information} : \mathbf{\Delta}_i = \mathbf{0} \end{cases}$$

Integration of one source

- Integration of external EBV and REL

$$\begin{bmatrix} \mathbf{X'R^{-1}X} & \mathbf{X'R^{-1}Z} \\ \mathbf{Z'R^{-1}X} & \mathbf{Z'R^{-1}Z + G^{*-1}} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_L \\ \hat{\mathbf{u}}_L \end{bmatrix} = \begin{bmatrix} \mathbf{X'R^{-1}y}_L \\ \mathbf{Z'R^{-1}y}_L \end{bmatrix}$$

$$\begin{bmatrix} \mathbf{X'R^{-1}X} & \mathbf{X'R^{-1}Z} \\ \mathbf{Z'R^{-1}X} & \mathbf{Z'R^{-1}Z + G^{*-1}} + \boldsymbol{\Lambda} \end{bmatrix} \begin{bmatrix} \hat{\boldsymbol{\beta}}_L \\ \hat{\mathbf{u}}_L \end{bmatrix} = \begin{bmatrix} \mathbf{X'R^{-1}y}_L \\ \mathbf{Z'R^{-1}y}_L + \mathbf{D^{-1}\hat{u}}_E \end{bmatrix}$$

Least square parts of LHS of the hypothetical BLUP

RHS of the hypothetical BLUP

Integration of one source: simulation

- 100 replicates
- 2 populations
  - ±1000 animals/population
  - 5 generations
  - Random matings / cullings
  - Observations (Van Vleck, 1994)
    - Milk yield for the first lactation
    - Heritability : 0.25
  - Fixed effect
    - Random herd effect within population

Integration of one source: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Bayesian BLUP	Joint BLUP
Pedigree				
External population	✓			
Local population + 50 external sires used locally				
Phenotypes				
External observations	✓			
Local observations				
50 external sires				
External EBV and REL				

Integration of one source: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Bayesian BLUP	Joint BLUP
Pedigree				
External population	✓			
Local population + 50 external sires used locally		✓		
Phenotypes				
External observations	✓			
Local observations		✓		
50 external sires				
External EBV and REL				

Integration of one source: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Bayesian BLUP	Joint BLUP
Pedigree				
External population	✓			
Local population		✓	✓	
+ 50 external sires used locally				
Phenotypes				
External observations	✓			
Local observations		✓	✓	
50 external sires				
External EBV and REL			✓	

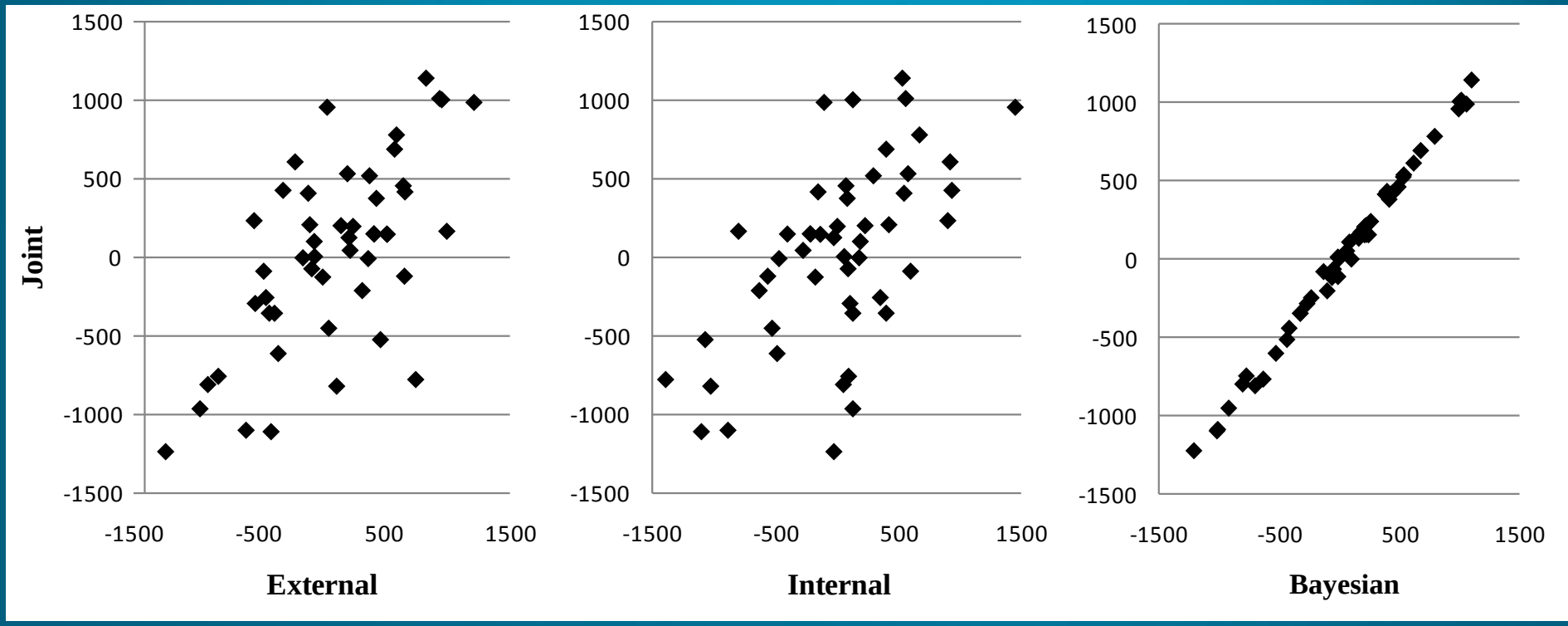
Integration of one source: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Bayesian BLUP	Joint BLUP
Pedigree				
External population	✓			✓
Local population + 50 external sires used locally		✓	✓	✓
Phenotypes				
External observations	✓			✓
Local observations		✓	✓	✓
50 external sires				
External EBV and REL			✓	

Comparison with joint BLUP

- EBV of the 50 external sires used locally



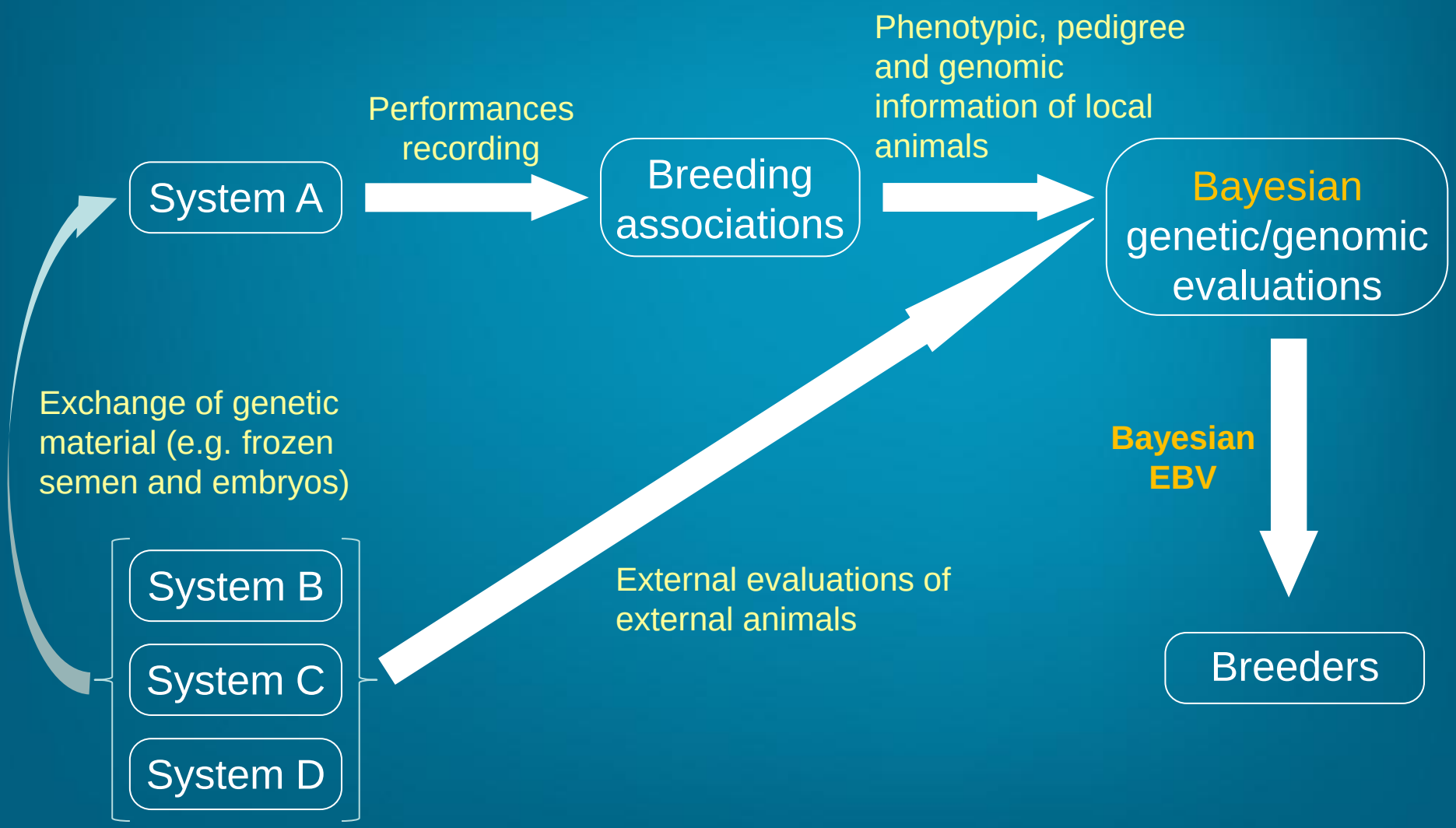
Comparison with joint BLUP

- Rank correlations (r) and mean squared errors (MSE) expressed as a percentage of the local MSE

Evaluation	Local animals		External sires	
	r ± SD	MSE ± SD	r ± SD	MSE ± SD
Without external information				
Local BLUP	0.95 ± 0.02	100.00 ± 33.5	0.54 ± 0.12	100.00 ± 28.2
With external information	>0.99 ± 0.000	0.79 ± 0.52	0.99 ± 0.002	0.49 ± 0.25

➔Rankings more similar to those of the joint BLUP

Integration of multiple sources



Integration of multiple sources

- Assumption: *A priori* known information of $\mathbf{u}_L$
  - *n* sources of external information:
    - *n* vector of external EBV

      $\hat{\mathbf{u}}_{E_1}, \ldots, \hat{\mathbf{u}}_{E_i}, \ldots, \hat{\mathbf{u}}_{E_n}$

    - *n* prediction error (co)variances matrices

      $\mathbf{D}_{E_1}, \ldots, \mathbf{D}_{E_i}, \ldots, \mathbf{D}_{E_n}$

  - Issue: only available for some animals

➔ $\hat{\mathbf{u}}_{E_i}$ and $\mathbf{D}_{E_i}$: (partially) unknown

Integration of multiple sources

- For each source *i*: Estimation of $\hat{\mathbf{u}}_{E_i}$
  - Available: External EBV of external animals ($\hat{\mathbf{u}}^{*}_{EE_i}$)
  - Local animals: prediction of external EBV ($\hat{\mathbf{u}}_{EL_i}$)

$$p(\hat{\mathbf{u}}_{EL_i} \mid \hat{\mathbf{u}}^{*}_{EE_i}) = MVN\left(\mathbf{G}_{LE_i}\mathbf{G}^{-1}_{EE_i}\hat{\mathbf{u}}^{*}_{EE_i}, (\mathbf{G}^{EE_i})^{-1}\right)$$

➔ $\hat{\mathbf{u}}_{E_i} = \begin{bmatrix} \hat{\mathbf{u}}_{EL_i} \\ \hat{\mathbf{u}}^{*}_{EE_i} \end{bmatrix}$

$\hat{\mathbf{u}}_{EL_i}$ → **Predicted external EBV**

$\hat{\mathbf{u}}^{*}_{EE_i}$ → **Available external EBV**

➔Correct propagation of external information

Integration of multiple sources

- For each source *i*: Estimation of $\mathbf{D}_{E_i}$

$$\mathbf{D}_{E_i}^{-1} = \mathbf{G}^{-1} + \mathbf{\Lambda}_{E_i}$$

$\mathbf{G}^{-1} = \mathbf{A}^{-1} \otimes \mathbf{G}_0^{-1}$: Inverse of genetic (co)variances matrix of $\hat{\mathbf{u}}_{E_i}$

$$\mathbf{\Lambda}_{E_i} = \text{block diag}(\mathbf{\Delta}_j \mathbf{G}_0^{-1} \mathbf{\Delta}_j);\ i = 1,..., n \text{ sources};\ j = 1,..., a \text{ animals}$$

$$\begin{cases} \text{For external animals}: \mathbf{\Delta}_j = \text{diag}\left(\sqrt{REL_{ijk} / (1 - REL_{ijk})}\right);\ k = 1,..., t \text{ traits} \\ \text{For animals with only local information}: \mathbf{\Delta}_j = \mathbf{0} \end{cases}$$

Integration of multiple sources

- Integration of *n* external information

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'R^{-1}y_L \\ Z'R^{-1}y_L \end{bmatrix}$$

$$\begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{*-1} + \sum_{i=1}^{n} \Lambda_{E_i} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'R^{-1}y_L \\ Z'R^{-1}y_L + \sum_{i=1}^{n} \left(D_{E_i}^{-1} \hat{u}_{E_i} \right) \end{bmatrix}$$

Sum of *n* least square parts of LHS of *n* hypothetical BLUP of *n* sources of external EBV

Sum of *n* RHS of *n* hypothetical BLUP of *n* sources of external EBV

Blending of multiple sources

- Blending of *n* external information
  - Assumption: no local records in $\mathbf{y}_L$

$$\left[\mathbf{G}^{*-1} + \sum_{i=1}^{n} \mathbf{\Lambda}_{E_i} \right] \hat{\mathbf{u}}_L = \left[\sum_{i=1}^{n} \left(\mathbf{D}_{E_i}^{-1} \hat{\mathbf{u}}_{E_i} \right) \right]$$

Issues

- Some issues arise before the implementation of a Bayesian evaluation like:
  - Compatibility between external and local traits
    - Same expression of external and local traits

    ➔Need to translate external information (e.g., using conversion equations (e.g., Vandenplas et al., 2012a))
  - Double counting of information
    - Due to relationships among external animals
    - Among external and local information
    - Among multiple external information

Issues

- Double counting due to relationships
  - The animal's EBV and REL combine contributions:
    - due to own records (if present)
    - due to relationships (Misztal and Wiggans, 1988)

➔Multiple considerations of parts of integrated external EBV for related external animals

➔Estimation of contributions due to relationships and due to own records through a two-step algorithm (Vandenplas and Gengler, 2012)

➔ All Λ_{E_i} only depend on contributions due to own records

Issues

- Double counting among external (and local) information
  - Each external information has to be free of local or other external information.
  - Ex.: Integration of MACE-EBV
    - Included local information

    ➔Estimation of external information free of local information:

$$\mathbf{D}_E^{-1}\hat{\mathbf{u}}_E = \mathbf{D}_M^{-1}\hat{\mathbf{u}}_M - \mathbf{D}_L^{*-1}\hat{\mathbf{u}}_L^*$$

Issues

- Integration of MACE-EBV

$$\begin{bmatrix} X'_L R^{-1} X_L & X'_L R^{-1} Z_L \\ Z'_L R^{-1} X_L & Z'_L R^{-1} Z_L + G^{*-1} + D_M^{-1} - D_L^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'_L R^{-1} y_L \\ Z'_L R^{-1} y_L + D_M^{-1} \hat{u}_M - D_L^{*-1} \hat{u}_L^* \end{bmatrix}$$

Issues

- Integration of MACE-EBV

$$\begin{bmatrix} X'_L R^{-1} X_L & X'_L R^{-1} Z_L \\ Z'_L R^{-1} X_L & Z'_L R^{-1} Z_L + G^{*-1} + D_M^{-1} - D_L^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'_L R^{-1} y_L \\ Z'_L R^{-1} y_L + D_M^{-1} \hat{u}_M - D_L^{*-1} \hat{u}_L^* \end{bmatrix}$$

Inverse of (combined genomic -) pedigree based (co)variances matrix

Issues

- Integration of MACE-EBV

$$\begin{bmatrix} X'_L R^{-1} X_L & X'_L R^{-1} Z_L \\ Z'_L R^{-1} X_L & Z'_L R^{-1} Z_L + G^{*-1} + D_M^{-1} - D_L^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'_L R^{-1} y_L \\ Z'_L R^{-1} y_L + D_M^{-1} \hat{u}_M - D_L^{*-1} \hat{u}_L^* \end{bmatrix}$$

Inverse of (combined genomic -) pedigree based (co)variances matrix

Inverse of prediction error (co)variances matrix of MACE-EBV

Issues

- Integration of MACE-EBV

$$\begin{bmatrix} X'_L R^{-1} X_L & X'_L R^{-1} Z_L \\ Z'_L R^{-1} X_L & Z'_L R^{-1} Z_L + G^{*-1} + D_M^{-1} - D_L^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'_L R^{-1} y_L \\ Z'_L R^{-1} y_L + D_M^{-1} \hat{u}_M - D_L^{*-1} \hat{u}_L^* \end{bmatrix}$$

Inverse of (combined genomic -) pedigree based (co)variances matrix

Inverse of prediction error (co)variances matrix of MACE-EBV

Inverse of prediction error (co)variances matrix of local EBV

Issues

- Integration of MACE-EBV

$$\begin{bmatrix} X_L' R^{-1} X_L & X_L' R^{-1} Z_L \\ Z_L' R^{-1} X_L & Z_L' R^{-1} Z_L + G^{*-1} + D_M^{-1} - D_L^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X_L' R^{-1} y_L \\ Z_L' R^{-1} y_L + D_M^{-1} \hat{u}_M - D_L^{*-1} \hat{u}_L^* \end{bmatrix}$$

Inverse of (combined genomic -) pedigree based (co)variances matrix

Inverse of prediction error (co)variances matrix of MACE-EBV

Inverse of prediction error (co)variances matrix of local EBV

RHS of an hypothetical BLUP of MACE-EBV

Issues

- Integration of MACE-EBV

$$\begin{bmatrix} X'_L R^{-1} X_L & X'_L R^{-1} Z_L \\ Z'_L R^{-1} X_L & Z'_L R^{-1} Z_L + G^{*-1} + D_M^{-1} - D_L^{*-1} \end{bmatrix} \begin{bmatrix} \hat{\beta}_L \\ \hat{u}_L \end{bmatrix} = \begin{bmatrix} X'_L R^{-1} y_L \\ Z'_L R^{-1} y_L + D_M^{-1} \hat{u}_M - D_L^{*-1} \hat{u}_L^* \end{bmatrix}$$

Inverse of (combined genomic -) pedigree based (co)variances matrix

Inverse of prediction error (co)variances matrix of MACE-EBV

Inverse of prediction error (co)variances matrix of local EBV

RHS of an hypothetical BLUP of MACE-EBV

RHS of an hypothetical BLUP of local EBV

Bayesian ssGBLUP: simulation

- 100 replicates
- 2 populations
  - ±1000 animals/population
  - 5 generations
  - Random matings / cullings
  - Observations (Van Vleck, 1994)
    - Milk yield for the first lactation
    - Heritability : 0.25
  - Fixed effect
    - Random herd effect within population

Bayesian ssGBLUP: simulation

- Performed evaluations

Information	External BLUP	Local ssGBLUP	Bayesian ssGBLUP	Joint ssGBLUP
Pedigree				
External population	✓			
Local population				
+ 50 external sires used locally				
Phenotypes				
External observations	✓			
Local observations				
50 external sires				
Genotypes				
External EBV and REL				

Bayesian ssGBLUP: simulation

- Performed evaluations

Information	External BLUP	Local ssGBLUP	Bayesian ssGBLUP	Joint ssGBLUP
Pedigree				
External population	✓			
Local population		✓		
+ 50 external sires used locally				
Phenotypes				
External observations	✓			
Local observations		✓		
50 external sires				
Genotypes		✓		
External EBV and REL				

Bayesian ssGBLUP: simulation

- Performed evaluations

Information	External BLUP	Local ssGBLUP	Bayesian ssGBLUP	Joint ssGBLUP
Pedigree				
External population	✓			
Local population		✓	✓	
+ 50 external sires used locally				
Phenotypes				
External observations	✓			
Local observations		✓	✓	
50 external sires				
Genotypes		✓	✓	
External EBV and REL			✓	

Bayesian ssGBLUP: simulation

- Performed evaluations

Information	External BLUP	Local ssGBLUP	Bayesian ssGBLUP	Joint ssGBLUP
Pedigree				
External population	✓			✓
Local population		✓	✓	✓
+ 50 external sires used locally				
Phenotypes				
External observations	✓			✓
Local observations		✓	✓	✓
50 external sires				
Genotypes		✓	✓	✓
External EBV and REL			✓	

Comparison with joint ssGBLUP

- Rank correlations (r+SD)

Evaluation	Local animals	External sires
Without external information		
Local ssGBLUP	**0.94 ± 0.02**	**0.52 ± 0.14**
With external information Bayesian ssGBLUP		
With double counting	**>0.99 ± 0.000**	**0.99 ± 0.01**
Without double counting	**>0.99 ± 0.000**	**0.99 ± 0.01**

➔Rankings more similar to those of the joint ssGBLUP

Comparison with joint ssGBLUP

- Mean squared errors (MSE+SD)
  - Expressed as a percentage of the local MSE

Evaluation	Local animals	External sires
Without external information		
Local ssGBLUP	**100.00 ± 32.8**	**100.00 ± 29.1**
With external information		
Bayesian ssGBLUP		
With double counting	**2.37 ± 2.2**	**1.35 ± 1.2**
Without double counting	**1.97 ± 2.1**	**1.12 ± 1.2**

➔ Importance of double-counting

Blending: simulation

- 100 replicates
- 2 populations
  - ±1000 animals/population
  - 5 generations
  - Random matings / cullings
  - Observations (Van Vleck, 1994)
    - Milk yield for the first lactation
    - Heritability : 0.25
  - Fixed effect
    - Random herd effect within population

Blending: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Blending BLUP	Joint BLUP
Pedigree				
External population	✓			
Local population + 50 external sires used locally				
Phenotypes				
External observations	✓			
Local observations				
External information				
External EBV and REL (50 external sires)				
Local EBV and REL (all population)				

Blending: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Blending BLUP	Joint BLUP
Pedigree				
External population	✓			
Local population + 50 external sires used locally		✓		
Phenotypes				
External observations	✓			
Local observations		✓		
External information				
External EBV and REL (50 external sires)				
Local EBV and REL (all population)				

Blending: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Blending BLUP	Joint BLUP
Pedigree				
External population	✓			
Local population + 50 external sires used locally		✓	✓	
Phenotypes				
External observations	✓			
Local observations		✓		
External information				
External EBV and REL (50 external sires)			✓	
Local EBV and REL (all population)			✓	

Blending: simulation

- Performed evaluations

Information	External BLUP	Local BLUP	Blending BLUP	Joint BLUP
Pedigree				
External population	✓			✓
Local population + 50 external sires used locally		✓	✓	✓
Phenotypes				
External observations	✓			✓
Local observations		✓		✓
External information				
External EBV and REL (50 external sires)			✓	
Local EBV and REL (all population)			✓	

Comparison with joint BLUP

- Rank correlations (r+SD)

Evaluation	Local animals	External sires
Without external information		
Local BLUP	**0.95 ± 0.02**	**0.54 ± 0.11**
Only external information Blending BLUP		
With double counting	**0.99 ± 0.004**	**0.97 ± 0.01**
Without double counting	**>0.99 ± 0.000**	**>0.99 ± 0.001**

➔ Rankings more similar to those of the joint BLUP

Comparison with joint BLUP

- Mean squared errors (MSE+SD)
  - Expressed as a percentage of the local MSE

Evaluation	Local animals	External sires
Without external information		
Local BLUP	**100.00 ± 26.7**	**100.00 ± 24.5**
Only external information Blending BLUP		
With double counting	**21.20 ± 6.2**	**6.83 ± 1.9**
Without double counting	**0.48 ± 0.2**	**0.23 ± 0.1**

➔ Importance of double counting

Conclusion

- Bayesian (ssG)BLUP
  - ➔Rankings most similar to those of a joint (ssG)BLUP
  - – Importance of double counting among animals

➔ Bayesian procedure

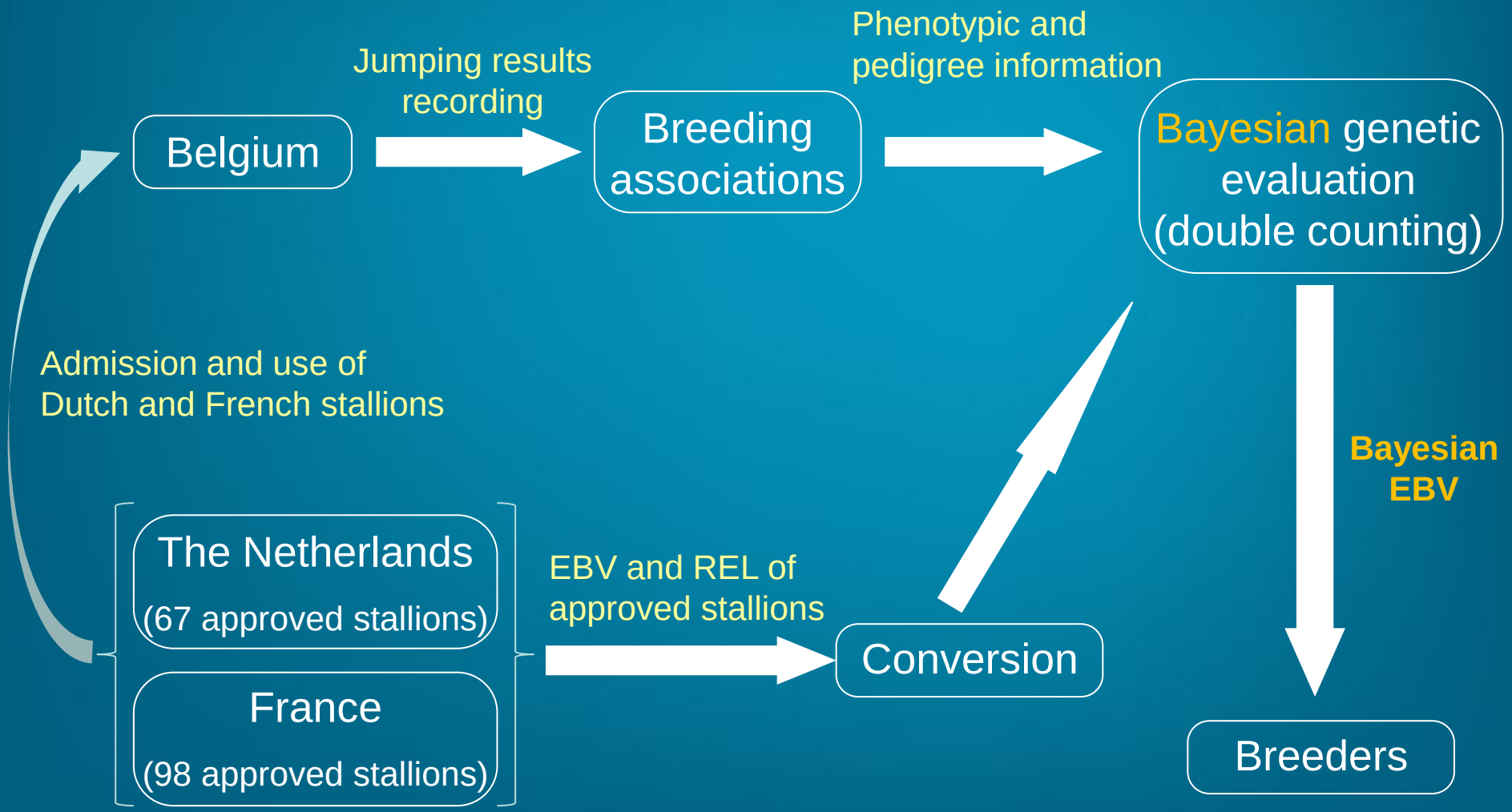
- – Reliable integration/blending of multiple external information
- – Simple modifications of current programs
- – Applicable to multi-traits models

Practical example: jumping horses

- Belgium = crossroad of sport horse populations
- 2008: >50% approved foreign stallions
- Export of sport horses
- Limited Belgian population (~ 4500 foals/year)

➔ Limited amount of information for reliable local EBV

Practical example: jumping horses



Practical example: jumping horses

- Spearman rank correlations

Group of horses	Nb	Spearman rank correlations		
		EBV_{AI} /EBV_{BI}	EBV_{AI} /EBV_{E}	EBV_{BI} /EBV_{E}
All horses	101,382	>0.99	-	-
French stallions	98	0.87	0.69	0.90
Dutch stallions	67	0.95	0.61	0.73

Practical example: jumping horses

- Reliabilities

Group of horses	Genetic evaluation[1]	Datasets[2]					
		I		II		III	
		Mean	SD	Mean	SD	Mean	SD
All horses	A	0.21	0.17	0.17	0.16	0.21	0.17
	B	0.21	0.17	0.17	0.16	0.21	0.17
French stallions	A	0.58	0.23	0.54	0.24	0.52	0.26
	B	0.61	0.20	0.58	0.20	0.57	0.21
Dutch stallions	A	0.51	0.26	0.46	0.26	0.47	0.27
	B	0.52	0.25	0.47	0.25	0.49	0.26

[1]A =Belgian genetic evaluation; B = Bayesian evaluation

[2]I = complete data; II = data for which all performances after December 31th, 2005 were assumed to be missing; III = data for which all French and Dutch stallions' own performances were assumed to be missing

Practical example: jumping horses

- Reliabilities

Group of horses	Genetic evaluation[1]	Datasets[2]					
		I		II		III	
		Mean	SD	Mean	SD	Mean	SD
All horses	A	0.21	0.17	0.17	0.16	0.21	0.17
	B	0.21	0.17	0.17	0.16	0.21	0.17
French stallions	A	0.58	0.23	0.54	0.24	0.52	0.26
	B	0.61	0.20	0.58	0.20	0.57	0.21
Dutch stallions	A	0.51	0.26	0.46	0.26	0.47	0.27
	B	0.52	0.25	0.47	0.25	0.49	0.26

[1]A =Belgian genetic evaluation; B = Bayesian evaluation

[2]I = complete data; II = data for which all performances after December 31th, 2005 were assumed to be missing; III = data for which all French and Dutch stallions' own performances were assumed to be missing

Practical example: jumping horses

- Reliabilities

Group of horses	Genetic evaluation[1]	Datasets[2]					
		I		II		III	
		Mean	SD	Mean	SD	Mean	SD
All horses	A	0.21	0.17	0.17	0.16	0.21	0.17
	B	0.21	0.17	0.17	0.16	0.21	0.17
French stallions	A	0.58	0.23	0.54	0.24	0.52	0.26
	B	0.61	0.20	0.58	0.20	0.57	0.21
Dutch stallions	**A**	**0.51**	**0.26**	**0.46**	**0.26**	**0.47**	**0.27**
	B	**0.52**	**0.25**	**0.47**	**0.25**	**0.49**	**0.26**

[1]A =Belgian genetic evaluation; B = Bayesian evaluation

[2]I = complete data; II = data for which all performances after December 31th, 2005 were assumed to be missing; III = data for which all French and Dutch stallions' own performances were assumed to be missing

Practical example: jumping horses

- Conclusions
  - External information partially to totally equivalent to 4 years of contemporary horses' performances or to their own performances
  - Resulting Belgian ranking more similar to foreign rankings
  - Improvement of REL

➔ Interesting for foreign stallions having no or few Belgian performances

Further work

- Integration of external genomic information
- Integration of correlated external information
  - ➔ To improve the accuracy of (ssG)BLUP for only locally available traits (e.g., fatty acids)

Thank you for your attention!

Corresponding author's e-mail: jvandenplas@ulg.ac.be

- Acknowledgments for financial support
  - National Fund for Scientific Research (FNRS), Belgium
  - Wallonie-Bruxelles International (WBI) and Government of the Republic of Slovenia (Slovenian Research Agency – ARRS) through bilateral cooperation agreement

- Acknowledgments for hosting
  - Dr Gregor Gorjanc, University of Ljubljana, Slovenia
  - Animal and Dairy Science Department, University of Georgia, Athens, USA

References

Legarra, A., J. K. Bertrand, T. Strabel, R. L. Sanchez, and I. Misztal. 2007. Multi-breed genetic evaluation in a Gelbvieh population. J. Anim. Breed. Genet. 124:286-295.

Quaas, R. L. and Z. Zhang. 2006. Multiple-breed genetic evaluation in the US beef cattle: methodology. CD-ROM Commun. 24-12 in Proc. 8th World Congr. Appl. Livest. Prod., Belo Horizonte, Brazil.

Vandenplas, J., P. Faux, I. Misztal, and N. Gengler. 2012a. Bayesian integration of external information into the single step approach for genomically enhanced prediction of breeding values. ADSA-AMPA-ASAS-CSAS-WSASAS Joint Annual Meeting. Phoenix (USA), 15-19 July 2012.

Vandenplas, J., and N. Gengler. 2012a. Comparison and improvements of different Bayesian procedures to integrate external information into genetic evaluations. J. Dairy Sci. 95:1513-1526.

Vandenplas, J., and N. Gengler. 2012b. Extension of Bayesian procedures to integrate and to blend multiple external information into genetic evaluations. ADSA-AMPA-ASAS-CSAS-WSASAS Joint Annual Meeting. Phoenix (USA), 15-19 July 2012.

Vandenplas, J., S. Janssens, N. Buys, and N. Gengler. 2012b. An integration of external information for foreign stallions into the Belgian genetic evaluation for jumping horses. J. Anim. Breed. Genet. Accepted.